

SEQUENCE LISTING

Mtb41 (MTCC#2)

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

GAGGTTGCTG GCAATGGATT TCGGGCTTTT ACCTCCGGAA GTGAATTCAA GCCGAATGTA      60
TTCCGGTCCG GGGCCGGAGT CGATGCTAGC CGCCGCGGCC GCCTGGGACG GTGTGGCCGC      120
GGAGTTGACT TCCGCCGCGG TCTCGTATGG ATCGGTGGTG TCGACGCTGA TCGTTGAGCC      180
GTGGATGGGG CCGGCGGCGG CCGCGATGGC GGCCGCGGCA ACGCCGTATG TGGGGTGGCT      240
GGCCGCCACG GCGGCGCTGG CGAAGGAGAC GGCCACACAG GCGAGGGCAG CGGCGGAAGC      300
GTTTGGGACG GCGTTCGCGA TGACGGTGCC ACCATCCCTC GTCGCGGCCA ACCGCAGCCG      360
GTTGATGTCG CTGGTCGCGG CGAACATTCT GGGGCAAAAC AGTGCGGCGA TCGCGGCTAC      420
CCAGGCCGAG TATGCCGAAA TGTGGGCCCC AGACGCTGCC GTGATGTACA GCTATGAGGG      480
GGCATCTGCG GCCGCGTCGG CGTTGCCGCC GTTCACTCCA CCCGTGCAAG GCACCGGCCC      540
GGCCGGGCCC GCGGCCGCGC CCGCGGCGAG CCAAGCCGCC GGTGCGGGCG CCGTTGCGGA      600
TGCACAGGCG ACACTGGCCC AGCTGCCCCC GGGGATCCTG AGCGACATTC TGTCCGCATT      660
GGCCGCCAAC GCTGATCCGC TGACATCGGG ACTGTTGGGG ATCGCGTCGA CCTCAACCC      720
GCAAGTCGGA TCCGCTCAGC CGATAGTGAT CCCCACCCCG ATAGGGGAAT TGGACGTGAT      780
CGCGCTCTAC ATTGCATCCA TCGCGACCGG CAGCATTGCG CTCGCGATCA CGAACACGGC      840
CAGACCCTGG CACATCGGCC TATACGGGAA CGCCGGCGGG CTGGGACCGA CGCAGGGCCA      900
TCCACTGAGT TCGGCGACCG ACGAGCCGGA GCCGCACTGG GGCCCCTTCG GGGGCGCGGC      960
GCCGGTGTCC GCGGGCGTCG GCCACGCAGC ATTAGTCGGA GCGTTGTCGG TGCCGCACAG     1020
CTGGACCACG GCCGCCCCGG AGATCCAGCT CGCCGTTTCA GCAACACCCA CCTTCAGCTC     1080
CAGCGCCGGC GCCGACCCGA CGGCCCTAAA GGGGATGCCG GCAGGCCTGC TCAGCGGGAT     1140
GGCTTTGGCG AGCCTGGCCG CACGCGGCAC GACGGGCGGT GGCGGCACCC GTAGCGGCAC     1200
CAGCACTGAC GGCCAAGAGG ACGGCCGCAA ACCCCCCGTA GTTGTGATTA GAGAGCAGCC     1260
GCCGCCCGGA AACCCCCCGC GGTAAAAGTC CGGCAACCGT TCGTCGCCGC GCGGAAAATG     1320
CCTGGTGAGC GTGGCTATCC GACGGGCGCT TCACACCGCT TGTAGTAGCG TACGGCTATG     1380
GACGACGGTG TCTGGATTCT CGGCGGCTAT CAGAGCGATT TTGCTCGCAA CCTCAGCAAA     1440
G

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1           5           10           15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp

```

		20						25						30					
Gly	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val				
		35					40					45							
Val	Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala				
	50					55					60								
Met	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala				
65					70					75					80				
Ala	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala				
				85					90					95					
Phe	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala				
			100					105					110						
Asn	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln				
		115					120					125							
Asn	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp				
	130					135					140								
Ala	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Glu	Gly	Ala	Ser	Ala	Ala				
145					150					155					160				
Ala	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro				
				165					170					175					
Ala	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly				
			180					185					190						
Ala	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile				
		195					200					205							
Leu	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr				
	210					215					220								
Ser	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser				
225					230					235					240				
Ala	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile				
			245						250					255					
Ala	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile				
			260					265					270						
Thr	Asn	Thr	Ala	Arg	Pro	Trp	His	Ile	Gly	Leu	Tyr	Gly	Asn	Ala	Gly				
		275					280					285							
Gly	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Glu				
	290					295					300								
Pro	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala				
305					310					315					320				
Gly	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser				
			325						330					335					
Trp	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro				
			340					345					350						
Thr	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met				
		355					360					365							
Pro	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu							

Mtb40 (HTCC#1)

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGCATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGATAC 60
ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT 120
TCGAAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCCGGG TGATGGCTGG TTAGGTTTCGG 180
CCGCGGACAA ATACGCCGGC AAAAACCAGCA ACCACGTGAA TTTTTCCTAG GAACTGGCAG 240
ACCTCGATCG TCAGCTCATC AGCCTGATCC ACGACCAGGC CAACGCGGTC CAGACGACCC 300
GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC 360
TGACCTACAT CCCGGTCGTC GGGCACGCCC TATCGGCCGC CTTCCAGGCG CCGTTTTGCG 420
CGGGCGCGAT GGCCGTAGTG GCGGCGCGCG TTGCCTACTT GGTCTGATAA ACGCTGATCA 480
ACGCGACTCA ACTCCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTCCGC GCCGCCATTG 540
CGGACATCAT TTCGGATGTG GCGGACATCA TCAAGGGCAC CCTCGGAGAA GTGTGGGAGT 600
TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA 660
CCGGACTGTT CTCTCGAGGG TGGTCGAACC TGGAGTCCTT CTTTGCGGGC GTCCCCGCT 720
TGACCGGCGC GACCAGCGGC TTGTCGAAG TGAAGTGGCT GTTCGGTTCG GCCGCTCTGT 780
CCGCATCGTC GGGCTTGGCT CACGCGGATA GCCTGGCGAG CTCAGCCAGC TTGCCCGCCC 840
TGGCCGGCAT TGGGGGCGGG TCCGGTTTTG GGGGCTTGCC GAGCCTGGCT CAGGTCCATG 900
CCGCCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCCGGTCGCG GCCCTGCCG 960
AGCAGGTCGG CGGGCAGTCG CAGCTGGTCT CCGCGCAGGG TTCCCAAGGT ATGGGCGGAC 1020
CCGTAGGCAT GGGCGGCATG CACCCCTCTT CCGGGGCGTC GAAAGGGACG ACGACGAAGA 1080
AGTACTCGGA AGGCGCGGCG GCGGGCACTG AAGACGCCGA GCGCGCGCCA GTCGAAGCTG 1140
ACGCGGGCGG TGGGCAAAAG GTGCTGGTAC GAAACGTCGT CTAACGGCAT GGCGAGCCAA 1200

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100 105 110

000001 " 4288960

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

Mtb9.9A (MTI-A)

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTCTCTT TCAACGTCAT AAGTTCGGTG GGCCAGTCGG CCGCGCGTGC ATATGGCACC
 AATAACGCGT GTCCCATGGA TACCCGGACC GCACGACGGT AGAGCGGATC AGCGCAGCCG

60
 120

GTGCCGAACA CTACCGCGTC CACGCTCAGC CCTGCCGCGT TGCGGAAGAT CGAGCCCAGG 180
 TTCTCATGGT CGTTAACGCC TTCCAACACT GCGACGGTGC GCGCCCCGGC GACCACCTGA 240
 GCAACGCTCG GCTCCGGCAC CCGGCGCGCG GCTGCCAACA CCCCACGATT GAGATGGAAG 300
 CCGATCACCC GTGCCATGAC ATCAGCCGAC GCTCGATAGT ACGGCGCGCC GACACCGGCC 360
 AGATCATCCT TGAGCTCGGC CAGCCGGCGG TCGGTGCCGA ACAGCGCCAG CGGCGTGAAC 420
 CGTGAGGCCA GCATGCGCTG CACCACCAGC ACACCCTCGG CGATACCAA CGCCTTGCCG 480
 GTCGGCAGAT CGGGACNACN GTCGATGCTG TTCAGGTCAC GGAAATCGTC GAGCCGTGGG 540
 TCGTCGGGAT CGCAGACGTC CTGAACATCG AGGCCGTCGG GGTGCTGGGC ACAACGGCCT 600
 TCGGTCACGG GCTTTCGTCG ACCAGAGCCA GCATCAGATC GGCGGCGCTG CGCAGGATGT 660
 CACGCTCGCT GCGGTTTCAGC GTCGCGAGCC GCTCAGCCAG CCACTCTTGC AGAGAGCCGT 720
 TGCTGGGATT AATTGGGAGA GGAAGACAGC ATGTCGTTTCG TGACCACACA GCCGGAAGCC 780
 CTGGCAGCTG CGGCGGCGAA CCTACAGGT ATTGGCACGA CAATGAACGC CCAGAACCGC 840
 GCCGCGGCTG CTCCAACCAC CGGAGTAGTG CCCGCAGCCG CCGATGAAGT ATCAGCGCTG 900
 ACCGCGGCTC AGTTTGCTGC GCACGCGCAG ATGTACCAA CCGTCAGCGC CCAGGCCCGC 960
 GCCATTACAG AAATGTTCTG GAACACGCTG GTGGCCAGTT CTGGCTCATA CGCGGCCACC 1020
 GAGGCGGCCA ACGCAGCCGC TGCCGGCTGA ACGGGCTCGC ACGAACCTGC TGAAGGAGAG 1080
 GGGGAACATC CGGAGTTCTC GGGTCAGGGG TTGCGCCAGC GCCCAGCCGA TTCAGNTATC 1140
 GGCGTCCATA ACAGCAGACG ATCTAGGCAT TCAGTACTAA GGAGACAGGC AACATGGCCT 1200
 CACGTTTTAT GACGGATCCG CATGCGATGC GGGACATGGC GGGCCGTTTT GAGGTGCACG 1260
 CCCAGACGGT GGAGGACGAG GCTCGCCGGA TGTGGGCGTC CGCGCAAAC ATTTCCGGTG 1320
 CGGGCTGGAG TGGCATGGCC GAGGCGACCT CGTAGACAC CATGACCTAG ATGAATCAGG 1380
 CGTTTTCGCAA CATCGTGAAC ATGCTGCACG GGGTGCCTGA CCGGCTGGTT CGCGACGCCA 1440
 ACAANTACGA ACAGCAAGAG CAGGCCTCCC AGCAGATCCT GAGCAGNTAG CGCCGAAAGC 1500
 CACAGCTGNG TACGNTTCT CACATTAGGA GAACACCAAT ATGACGATTA ATTACCAGTT 1560
 CGGGGACGTC GACGCTCATG GCGCCATGAT CCGCGCTCAG GCGGCGTCGC TTGAGGCGGA 1620
 GCATCAGGCC ATCGTTCTGT ATGTGTTGGC CCGGGGTGAC TTTTGGGGCG GCGCCGGTTC 1680
 GGTGGCTTGC CAGGAGTTCA TTACCCAGTT GGGCCGTAAC TTCCAGGTGA TCTACGAGCA 1740
 GG 1742

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTGATTCCG TTCGCGGCGC CGCCGAAGAC CACCAACTCC GCTGGGGTGG TCGCACAGGC 60
 GGTTGCGTCG GTCAGCTGGC CGAATCCCAA TGATTGGTGG CTCNGTGCGG TTGCTGGGCT 120
 CGATTACCCC CACGGAAAGG ACGACGATCG TTCGTTTGCT CCGTCAGTCG TACTTGCGGA 180
 CGGGCATGGC GCGGTTTCTT ACCTCGATCG CACAGCAGCT GACCTTCGGC CCAGGGGGCA 240
 CAACGGCTGG CTCCGGCGGA GCCTGGTACC CAACGCCACA ATTCGCCGGC CTGGGTGCAG 300
 GCGGCGCGGT GTCGCGGAGT TTGGCGCGGG CGGAGCCGGT CCGGAGGTTG TCGGTGCCGC 360
 CAAGTTGGGC CGTCGCGGCT CCGGCCTTCG CGGAGAAGCC TGAGGCGGGC ACGCCGATGT 420
 CCGTCATCGG CGAAGCGTCC AGCTGCGGTC AGGGAGGCCT GCTTCGAGGC ATACCGCTGG 480
 CGAGAGCGGG GCGGCGTACA GCGCCTTCG CTCACCGATA CGGGTTCCGC CACAGCGTGA 540
 TTACCCGGTC TCGTCGGCGG GGATAGCTTT CGATCCGGTC TGCGCGGCCG CCGGAAATGC 600
 TGCAGATAGC GATCGACCGC GCCGGTCGGT AAACGCCGCA CACGGCACTA TCAATGCGCA 660
 CGGCGGGCGT TGATGCCAAA TTGACCGTCC CGACGGGGCT TTATCTGCGG CAAGATTTCA 720
 TCCCCAGCCC GGTCGGTGGG CCGATAAATA CGCTGGTCAG CGCGACTCTT CCGGCTGAAT 780

09688672-101000

TCGATGCTCT	GGGCGCCCGC	TCGACGCCGA	GTATCTCGAG	TGGGCCGCAA	ACCCGGTCAA	840
ACGCTGTTAC	TGTGGCGTTA	CCACAGGTGA	ATTTGCGGTG	CCAAGTGGTG	AACACTTGCG	900
AACGGGTGGC	ATCGAAATCA	ACTTGTTCG	TTGCAGTGAT	CTACTCTCTT	GCAGAGAGCC	960
GTTGCTGGGA	TTAATTGGGA	GAGGAAGACA	GCATGTCGTT	CGTGACCACA	CAGCCGGAAG	1020
CCCTGGCAGC	TGCGGCGGCG	AACCTACAGG	GTATTGGCAC	GACAATGAAC	GCCGAGAACG	1080
CGGCCGCGGC	TGCTCCAACC	ACCGGAGTAG	TGCCCCGAGC	CGCCGATGAA	GTATCAGCGC	1140
TGACCGCGGC	TCAGTTTGCT	GCGCACGCGC	AGATGTACCA	AACGGTCAGC	GCCGAGGCCG	1200
CGGCCATTCA	CGAAATGTTT	GTGAACACGC	TGGTGGCCAG	TTCTGGCTCA	TACGCGGCCA	1260
CCGAGGCGGC	CAACGCAGCC	GCTGCCGGCT	GAACGGGCTC	GCACGAACCT	GCTGAAGGAG	1320
AGGGGGAACA	TCCGGAGTTC	TCGGGTCAGG	GGTTGCGCCA	GCGCCCAGCC	GATTGAGCTA	1380
TCGGCGTCCA	TAACAGCAGA	CGATCTAGGC	ATTCAGTACT	AAGGAGACAG	GCAACATGGC	1440
CTCACGTTTT	ATGACGGATC	CGCATGCGAT	GCGGGACATG	GCGGGCCGTT	TTGAGGTGCA	1500
CGCCCAGACG	GTGGAGGACG	AGGCTCGCCG	GATGTGGGCG	TCCGCGCAAA	ACATTTCCGG	1560
TGCGGGCTGG	AGTGGCATGG	CCGAGGCGAC	CTCGCTAGAC	ACCATGACCT	AGATGAATCA	1620
GGCGTTTCGC	AACATCGTGA	ACATGCTGCA	CGGGGTGCGT	GACGGGCTGG	TTGCGGACGC	1680
CAACAACCTAC	GAACAGCAAG	AGCAGGCCTC	CCAGCAGATC	CTGAGCAGCT	AGCGCCGAAA	1740
GCCACAGCTG	CGTACGCTTT	CTCACATTAG	GAGAACACCA	ATATGACGAT	TAATTACCAG	1800
TTGCGGGACG	TCGACGCTCA	TGGCGCCATG	ATCCGCGCTC	AGGCGGCGTC	GCTTGAGGCG	1860
GAGCATCAGG	CCATCGTTTC	TGATGTGTTG	GCCGCGGGTG	ACTTTTGGGG	CGGCGCCGGT	1920
TCGGTGGCTT	GCCAGGAGTT	CATTACCCAG	TTGGGCCGTA	ACTTCCAGGT	GATCTACGAG	1980
CAGGCCAACG	CCCACGGGCA	GAAGGTGCAG	GCTGCCGGCA	ACAACATGGC	GCAAACCGAC	2040
AGCGCCGTCG	GCTCCAGCTG	GGCCTAAAAC	TGAAGTTCAG	TCGCGGCAGC	ACACCAACCA	2100
GCCGGTGTGC	TGCTGTGTCC	TGCAGTTAAC	TAGCACTCGA	CCGCTGAGGT	AGCGATGGAT	2160
CAACAGAGTA	CCCGCACCGA	CATCACCGTC	AACGTCGACG	GCTTCTGGAT	GCTTCAGGCG	2220
CTACTGGATA	TCCGCCACGT	TGCGCCTGAG	TTACGTTGCC	GGCCGTACGT	CTCCACCGAT	2280
TCCAATGACT	GGGTCAAACG	GCACCCGGGG	ATGGCGGTCA	TGCGCGAGCA	GGGCATTGTC	2340
GTCAACGACG	CGGTCAAACG	ACAGGTGCGT	GCCCGGATGA	AGGTGCTTGC	CGCACCTGAT	2400
CTTGAAGTCG	TCGCCCTGCT	GTCACGCGGC	AAGTTGCTGT	ACGGGGTCAT	AGACGACGAG	2460
AACCAGCCGC	CGGGTTCGCG	TGACATCCCT	GACAATGAGT	TCCGGGTGGT	GTTGGCCCGG	2520
CGAGGCCAGC	ACTGGGTGTC	GGCGGTACGG	GTTGGCAATG	ACATCACCGT	CGATGACGTG	2580
ACGGTCTCGG	ATAGCGCCTC	GATCGCCGCA	CTGGTAATGG	ACGGTCTGGA	GTCGATTAC	2640
CACGCCGACC	CAGCCGCGAT	CAACGCGGTC	AACGTGCCAA	TGGAGGAGAT	CTCGTGCCGA	2700
ATTGCGCACG	AGGCACGAGG	CGGTGTCGGT	GACGACGGGA	TCGATCACGA	TCATCGACCG	2760
GCCGGGATCC	TTGGCGATCT	CGTTGAGCAC	GACCCGGGCC	CGCGGGAAGC	TCTGCGACAT	2820
CCATGGGTTT	TTCCCG					2836

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
1			5				10						15		
Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile
		20					25						30		
Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
		35					40						45		

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

09688672-101000

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
 1 5 10 15
 Gln Ala

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids

0963332 : 101000

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 15 amino acids

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: peptide

(A) ORGANISM: *Mycobacterium tuberculosis*

(2) INFORMATION FOR SEQ ID NO:65:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

Mtb9.8 (MSL)

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGATTCCGA TAGCGGTTTC GGCCCTCGA CGGGCGACCA CGGCGCGCAG GCCTCCGAAC 60
GGGGGGCCGG GACGCTGGGA TTCGCCGGA CCGCAACCA AGAACGCCGG GTCCGGGCGG 120
TCGGGCTGAC CGCACTGGCC GGTGATGAGT TCGGCAACGG CCCC CGGATG CCGATGGTGC 180
CGGGGACCTG GGAGCAGGGC AGCAACGAGC CCGAGGCGCC CGACGGATCG GGGAGAGGGG 240
GAGGCGACGG CTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCACGT GGACCCGTAC 300
GGGTGCGAAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCCACAG TTGGTGGCCT 360
CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCGGCA CACGATCGGT CAGGCCGAGC 420
AGGCGGCGAT GTCGGCTCAG GCGTTTCACC AGGGGGAGTC GTCGGCGGCG TTTCAGGCCG 480
CCCATGCCCC GTTTGTGGCG GCGGCCGCA AAGTCAACAC CTTGTTGGAT GTCGCGCAGG 540
CGAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTG 585

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser

35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

Mtb9.8 ORF peptides

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

09582672-171077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
1 5 10 15
Asp Ala

Mtb39A (TbH9)

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT 60
GGCATAACCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC 120
TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA 180
TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT 240
GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG 300
CTCGTATGCG GCCACTGAAG TCGCCAATGC GCGGCGGCGC AGCTAAGCCA GGAACAGTCG 360
GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGG TTTTCGGGCG TTACCACCGG 420
AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCGGCTC 480
AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTTCGGCCG GTCGGCGTTT CAGTCGGTGG 540
TCTGGGGTCT GACGGTGGGG TCGTGATAG GTTCGTGGC GGGTCTGATG GTGGCGGCGG 600
CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCCG 660
AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCCG 720
TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA 780
ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG 840
CCGCGATGTT TGGCTACGCC GCGGCGACGG CGACGGCGAC GGCGACGTTG CTGCCGTTCT 900
AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTGAGG 960
AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC 1020
AGCTGGCCCA GCCCACGCAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA 1080
CGGTCTCGCC GCATCGGTCT CCGATCAGCA ACATGGTGTG GATGGCCAAC AACCACATGT 1140
CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG 1200
CTCCGGCGGC GGCCGCCCAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA 1260
GCTCGCTGGG CAGCTCGCTG GGTCTTCGG GTCTGGGCGG TGGGGTGGCC GCCAACTTGG 1320
GTCGGGCGGC CTCGGTCTGG TCGTTGTCTG TGCCGCGAGC CTGGGCGCGG GCCAACCAGG 1380
CAGTCACCCG GGCGGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG 1440
GGCCCGGGCA GATGCTGGGC GGGCTGCCCG TGGGGCAGAT GGGCGCCAGG GCCGGTGGTG 1500
GGCTCAGTGG TGTGCTGCGT GTTCCGCGCG GACCCTATGT GATGCCGCAT TCTCCGGCGG 1560
CCGGCTAGGA GAGGGGGCGC AGACTGTCTG TATTGACCA GTGATCGGCG GTCTCGGTGT 1620
TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG 1680
GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG 1740
GGACATGGCG GGCCGTTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT 1800
GTGGGCGTCC GCGCAAAACA TTTCCGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC 1860
GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGTCGACCG 1920
GGTGCCTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA 1980
GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGACAAT ACTTTTACAA GCGAAGGAGA 2040
ACAGGTTTCA TGACCATCAA CTATCAATTC GGGGATGTCT ACGCTCACGG CGCCATGATC 2100
CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTCTGTA TGTGTTGACC 2160
GCGAGTGACT TTTGGGGCGG CGCCGGTTCT GCGGCCTGCC AGGGGTTTAT TACCCAGTTG 2220

GGCCGTA	ACT	TCCAGGT	GAT	CTACGAG	CAG	GCCAACG	CCCC	ACGGGCAG	AA	GGTGCAG	GCT	2280
GCCGGCA	ACA	ACATGGG	CGCA	AACCGAC	AGC	GCCGT	CGGCT	CCAGCTGG	GC	CTGACAC	CAG	2340
GCCAAGG	CCA	GGGACGT	GGT	GTACGAG	TGA	AGTTCCT	CGC	GTGATCCT	TTC	GGGTGGC	CAGT	2400
CTAAGTG	GTC	AGTGCTG	GGG	TGTTGGT	GGT	TTGCTGCT	TG	GCGGGTTCT	T	CGGTGCT	GGT	2460
CAGTGCT	GCT	CGGGCTC	GGG	TGAGGAC	CTC	GAGGCCA	G	TAGCGCCG	TTC	CTTCGAT	CCA	2520
TTCGTCG	TGT	TTCGGCG	GA	GGACGGC	TCC	GACGAGG	CGG	ATGATCG	GAG	CGCGGT	CGG	2580
GAAGATG	CCC	ACGACGT	CGG	TTCGGCG	TCG	TACCTCT	CGG	TTGAGGC	GTT	CCTGGGG	GTT	2640
GTTGGAC	CAG	ATTTGGC	GCC	AGATCTG	GCTT	GGGGAAG	GCG	GTGAACG	CCA	GCAGGT	CGGT	2700
GCGGGCG	GTTG	TCGAGGT	GCT	CGGCCAC	CGC	GGGGAGT	TTG	TCGGTCAG	AG	CGTCGAG	TAC	2760
CCGATCA	TAT	TGGGCA	ACAA	CTGATTC	CGC	GTCGGG	GCTGG	TCGTAGAT	G	AGTGCAG	CAG	2820
GGTGC	GCACC	CACGGCC	CAGG	AGGGCTT	CGG	GGTGGG	GCTGCC	ATCAGATT	G	CTGCGTA	G	2880
GGTTCTG	CAG	CGCTGCC	CAGG	CCGCTGC	GGG	CAGGGT	GCGC	CCGATCG	CGG	CCACCAG	GCC	2940
GGCGTG	GGCG	TCGCTGG	TGA	CCAGCGC	GAC	CCCGGAC	AGG	CCGCGGG	CGA	CCAGGT	CGC	3000
GAAGA	ACGCC	AGCCAGC	CGG	CCCCGTC	CCTC	GGCGGAG	G	ACCTGGAT	G	CCAGGAT	C	3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
1				5					10					15	
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp
			20					25					30		
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser
		35				40					45				
Val	Val	Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly
	50				55				60						
Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr
65				70					75					80	
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala
			85					90					95		
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala
			100				105						110		
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly
		115				120					125				
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met
	130					135					140				
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala
145				150					155					160	
Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr
				165					170					175	

000107-2988960

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
195 200 205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
210 215 220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
225 230 235 240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
245 250 255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
260 265 270

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

Mtb32A (TbRa35)

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG GTGTAGAAAA ATCCTGCCGC CCGGACCCTT AAGGCTGGGA CAATTTCTGA

60

115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

Mtb8.4 (DPV)

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG TCGTTGACCG TCGGGGCCCG GGTGCCTCC GCAGATCCCG TGGACGCGGT	60
CATTAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG	120
GGCTGCCGCA CAGTTCAACG CCTCACCAGT GCGCAGTCC TATTGCGCA ATTTCTCTCGC	180
CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC	240
ACAGTACATC GGCCTGTGCG AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC	300
GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA	360
ACGGGCGGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCCCCTCCT	420
CAACGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG	480
GCCGCCACCG CCGTGGAGCT	500

(2) INFORMATION FOR SEQ ID NO:102:

090907Z 101000

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Mtb11 (Tb38-1)

- (i) .SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCACGAGA | GACCGATGCC | GCTACCCTCG | CGCAGGAGGC | AGGTAATTTT | GAGCGGATCT | 60 |
| CCGGCGACCT | GAAAACCCAG | ATCGACCAGG | TGGAGTCGAC | GGCAGGTTCT | TTGCAGGGCC | 120 |
| AGTGGCGCGG | CGCGGCGGGG | ACGGCCGCCC | AGGCCGCGGT | GGTGCGCCTC | CAAGAAGCAG | 180 |
| CCAATAAGCA | GAAGCAGGAA | CTCGACGAGA | TCTCGACGAA | TATTCGTCTC | GCCGGCGTCC | 240 |
| AATACTCGAG | GGCCGACGAG | GAGCAGCAGC | AGGCGCTGTC | CTCGCAAATG | GGCTTCTGAC | 300 |
| CCGCTAATAC | GAAAAGAAAC | GGAGCAA | | | | 327 |

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly

20 25 30
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45
 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80
 Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

TbRa3

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGAACAGGC 60
 GCGGCGGAG GCGGTCCAGC GGGCGCGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT 120
 CATTGAGCAG GACATGGCCG TGGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA 180
 AGTGTCTGTT AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCCGGCGA GCAAGACGCA 240
 AAATCGCACG GTTTGCGGTT GATTCGTGCG ATTTTGTGTC TGCTCGCCGA GGCCTACCAG 300
 GCGGCGCCCA GGTCCGCGTG CTGCCGTATC CAGGCGTGCA TCGCGATTCC GCGGCGCCAG 360
 CCGGAGTTAA TGCTTCGCGT CGACCCGAAC TGGGCGATCC GCCGNGAGC TGATCGATGA 420
 CCGTGGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGTTAGGA 480
 AGCGTCCGTA GCGGCGCGTG CTGACCGGCT CTGCCTGCGC CCTCAGTGCG GCCAGCGAGC 540
 GG 542

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
 1 5 10 15
 Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
 20 25 30
 Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60
 Pro Arg
 65

38kD

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTC TCCTCGCCGA 60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC 120
GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAAATT CGTTTGCATA CGCTGTTGGC 180
CGTGTTGACC GCTGCGCCGC TGCTGCTAGC AGCGCGCGGC TGTGGCTCGA AACCACCGAG 240
CGGTTTCGCTT GAAACGGGCG CCGGCGCCCG TACTGTGCGG ACTACCCCG CGTCGTCGCC 300
GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC 360
GGCCTTTTAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC 420
CGGGATCGCG CAGGCGCGCG CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC 480
GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA 540
GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAAGTCCT 600
GGCGGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA 660
CCCCGGCGTG AACCTGCCCG GCACCGCGGT AGTTCGCTG CACCGCTCCG ACGGGTCCGG 720
TGACACCTTC TTGTTACCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC 780
GCCCCGCTTC GGCACCACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG 840
CAACGGCGGC ATGGTGACCG GTTGCGCCGA GACACCGGGC TCGGTGGCCT ATATCGGCAT 900
CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCAACTAG GCAATAGCTC 960
TGGCAATTTT TTGTTGCCCG ACGCGCAAAG CATTACAGGC GCGGCGGCTG GCTTCGCATC 1020
GAAAACCCCG GCGAACCAGG CGATTTTCAT GATCGACGGG CCCGCCCCGG ACGGCTACCC 1080
GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCCG CCACCGCGCA 1140
GACCTTGACG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAAGGCCT CGTTCCTCGA 1200
CCAGGTTTAT TTCCAGCCGC TGCCGCCCGG GGTGGTGAAG TTGTCTGACG CGTTGATCGC 1260
GACGATTTCC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG 1320
GCTGCTTTGC GGAGCATGCT GGCCCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC 1380
CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG 1440
GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTTGCATTT CTTACCGGCC 1500
ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC 1560
CGGTCGGCGC CTACTACGGG GCGTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA 1620
TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA 1740
GCGTGGTTCG CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800
CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTG GCGGGTGATG GTCGTTCCCA 1920
TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCC CGGGAGGGCG 1980
CGATCGGGAA TTC 1993

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

000001-298866

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220

Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255

Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285

Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320

Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335

His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365

Ile Ala Thr Ile Ser Ser
 370

DPEP

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC	ATCACCATCA	CATGCATCAG	GTGGACCCCA	ACTTGACACG	TCGCAAGGGA	60
CGATTGGCGG	CACTGGCTAT	CGCGGCGATG	GCCAGCGCCA	GCCTGGTGAC	CGTTGCGGTG	120
CCCGCGACCG	CCAACGCCGA	TCCGGAGCCA	GCGCCCCCGG	TACCCACAAC	GGCCGCCTCG	180
CCGCCGTCGA	CCGCTGCAGC	GCCACCCGCA	CCGGCGACAC	CTGTTGCCCC	CCCACCACCG	240
GCCGCCGCCA	ACACGCCGAA	TGCCAGCCG	GCGATCCCA	ACGCAGCACC	TCCGCCGGCC	300
GACCCGAACG	CACCGCCGCC	ACCTGTCATT	GCCCCAAACG	CACCCCAACC	TGTCCGGATC	360
GACAACCCGG	TTGGAGGATT	CAGCTTCGCG	CTGCCTGCTG	GCTGGGTGGA	GTCTGACGCC	420
GCCCCATTCT	ACTACGGTTC	AGCACTCCTC	AGCAAAACCA	CCGGGGACCC	GCCATTTCCC	480
GGACAGCCGC	CGCCGGTGCG	CAATGACACC	CGTATCGTGC	TCGGCCGGCT	AGACCAAAAG	540
CTTTACGCCA	GCGCCGAAGC	CACCGACTCC	AAGGCCGCGG	CCCGGTTGGG	CTCGGACATG	600
GGTGAGTTCT	ATATGCCCTA	CCCGGGCACC	CGGATCAACC	AGGAAACCGT	CTCGCTCGAC	660
GCCAACGGGG	TGTCTGGAAG	CGCGTCGTAT	TACGAAGTCA	AGTTCAGCGA	TCCGAGTAAG	720
CCGAACGGCC	AGATCTGGAC	GGCGTAATC	GGCTCGCCCG	CGGCGAACGC	ACCGGACGCC	780
GGGCCCCCTC	AGCGCTGGTT	TGTGGTATGG	CTCGGGACCG	CCAACAACCC	GGTGGACAAG	840
GGCGCGGCCA	AGGCGCTGGC	CGAATCGATC	CGGCCTTTGG	TCGCCCCGCC	GCCGGCGCCG	900
GCACCGGCTC	CTGCAGAGCC	CGCTCCGGCG	CCGGCGCCGG	CCGGGGAAGT	CGCTCCTACC	960
CCGACGACAC	CGACACCGCA	GCGGACCTTA	CCGGCCTGA			999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

09688672-101000

Met	His	His	His	His	His	His	Met	His	Gln	Val	Asp	Pro	Asn	Leu	Thr
1				5					10					15	
Arg	Arg	Lys	Gly	Arg	Leu	Ala	Ala	Leu	Ala	Ile	Ala	Ala	Met	Ala	Ser
			20					25					30		
Ala	Ser	Leu	Val	Thr	Val	Ala	Val	Pro	Ala	Thr	Ala	Asn	Ala	Asp	Pro
		35					40					45			
Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr
	50					55					60				
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro
65					70					75					80
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala
			85					90					95		
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro
			100					105					110		
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser
	115						120					125			
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His	Phe	Asp
	130				135						140				
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro
145					150					155					160
Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Leu	Gly	Arg
				165					170					175	
Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser	Lys	Ala
		180						185					190		
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro	Tyr	Pro
		195					200					205			
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn	Gly	Val
	210					215					220				
Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
225					230					235					240
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
			245					250					255		
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
		260					265						270		
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Glu
	275					280						285			
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro
	290					295				300					
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr
305				310				315							320
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala				
			325					330							

TbH4

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC

60

CGAGGAAAGC	CGCTACCAGA	TGGCGCTGCC	GAAGTAGGGC	GATCCGTTTCG	CGATGCCGGC	120
ATGAACGGGC	GGCATCAAAT	TAGTGCAGGA	ACCTTTTCAGT	TTAGCGACGA	TAATGGCTAT	180
AGCACTAAGG	AGGATGATCC	GATATGACGC	AGTCGCAGAC	CGTGACGGTG	GATCAGCAAG	240
AGATTTTGAA	CAGGGCCAAC	GAGGTGGAGG	CCCCGATGGC	GGACCCACCG	ACTGATGTCC	300
CCATCACACC	GTGCGAATC	ACGNGGGNTA	AAAACGCCGC	CCAACAGNTG	GTNTTGTCCG	360
CCGACAACAT	GCGGGAATAC	CTGGCGGCCG	GTGCCAAAGA	GCGGCAGCGT	CTGGCGACCT	420
CGCTGCGCAA	CGCGGCCAAG	GNGTATGGCG	AGGTTGATGA	GGAGGCTGCG	ACCGCGCTGG	480
ACAACGACGG	CGAAGGAACT	GTGCAGGCAG	AATCGGCCGG	GGCCGTCGGA	GGGGACAGTT	540
CGGCCGAAC	AACCGATACG	CCGAGGGTGG	CCACGGCCGG	TGAACCCAAC	TTCATGGATC	600
TCAAAGAAGC	GGCAAGGAAG	CTCGAAACGG	GCGACCAAGG	CGCATCGCTC	GCGCACTGNG	660
GGGATGGGTG	GAACACTTNC	ACCCTGACGC	TGCAAGGCCA	CG		702

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val
1				5					10					15	
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln
			20					25					30		
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val
			35				40					45			
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Xaa	Glu
		50				55				60					
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	Phe
65				70					75					80	
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	Glu
			85					90					95		
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala
			100				105						110		
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Xaa	Gln	Ile	Leu	Ala	Ser	Gly	Val
		115				120						125			
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp
		130			135					140					
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn
145				150				155						160	
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg
			165					170					175		
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly
			180				185					190			
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile
		195				200					205				
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Phe
		210			215					220					
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp
225				230					235					240	
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg
			245				250					255			
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
		260				265						270			
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Gly	Leu	Arg	Pro	Xaa	Lys		

MTbRa12

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC	ACGGCCGCGT	CCGATAACTT	CCAGCTGTCC	CAGGGTGGGC	AGGGATTTCGC	60
CATTCCGATC	GGGCAGGCGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GGGGGTCACC	120
CACCGTTCAT	ATCGGGCCTA	CCGCCTTCTT	CGGCTTGGGT	GTTGTCGACA	ACAACGGCAA	180
CGGCGCACGA	GTCCAACGCG	TGGTCGGGAG	CGCTCCGGCG	GCAAGTCTCG	GCATCTCCAC	240
CGGCGACGTG	ATCACC GCGG	TCGACGGCGC	TCCGATCAAC	TCGGCCACCG	CGATGGCGGA	300
CGCGCTTAAC	GGGCATCATC	CCGGTGACGT	CATCTCGGTG	AACTGGCAAA	CCAAGTCGGG	360
CGGCACGCGT	ACAGGGAACG	TGACATTGGC	CGAGGGACCC	CCGGCCTGAT	TTCGTCGYGG	420
ATACCACCCG	CCGGCCGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gly	Gln	Gly	Phe
1				5				10					15		
Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Arg	Ser
		20					25					30			
Gly	Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly
		35				40					45				
Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val
	50				55				60						
Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr	Gly	Asp	Val
65			70						75				80		
Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr	Ala	Met	Ala
		85					90					95			
Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Asn	Trp
		100					105					110			
Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu
		115				120						125			
Gly	Pro	Pro	Ala												
		130													

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAAGTTGA	AGTTTGCTCG	CCTGAGTACT	GCGATACTGG	GTTGTGCAGC	GGCGCTTGTG	60
TTTCCTGCCT	CGGTTGCCAG	CGCAGATCCA	CCTGACCCGC	ATCAGCCGGA	CATGACGAAA	120
GGCTATTGCC	CGGGTGGCCG	ATGGGGTTTT	GGCGACTTGG	CCGTGTGCGA	CGGCGAGAAG	180
TACCCCGACG	GCTCGTTTTG	GCACCAGTGG	ATGCAAACGT	GGTTTACCGG	CCCACAGTTT	240
TACTTCGATT	GTGTCAGCGG	CGGTGAGCCC	CTCCCCGGCC	CGCCGCCACC	GGGTGGTTGC	300
GGTGGGGCAA	TTCCGTCCGA	GCAGCCCAAC	GCTCCCTGA			339

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met	Lys	Leu	Lys	Phe	Ala	Arg	Leu	Ser	Thr	Ala	Ile	Leu	Gly	Cys	Ala
1				5					10					15	
Ala	Ala	Leu	Val	Phe	Pro	Ala	Ser	Val	Ala	Ser	Ala	Asp	Pro	Pro	Asp
		20					25						30		
Pro	His	Gln	Pro	Asp	Met	Thr	Lys	Gly	Tyr	Cys	Pro	Gly	Gly	Arg	Trp
		35				40						45			
Gly	Phe	Gly	Asp	Leu	Ala	Val	Cys	Asp	Gly	Glu	Lys	Tyr	Pro	Asp	Gly
		50			55					60					
Ser	Phe	Trp	His	Gln	Trp	Met	Gln	Thr	Trp	Phe	Thr	Gly	Pro	Gln	Phe
		65			70				75					80	
Tyr	Phe	Asp	Cys	Val	Ser	Gly	Gly	Glu	Pro	Leu	Pro	Gly	Pro	Pro	Pro
			85				90						95		
Pro	Gly	Gly	Cys	Gly	Gly	Ala	Ile	Pro	Ser	Glu	Gln	Pro	Asn	Ala	Pro
		100					105						110		

ESAT-6

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid

ATGACAGAGC	AGCAGTGGAA	TTTCGCGGGT	ATCGAGGCCG	CGGCAAGCGC	AATCCAGGGA	60
AATGTCACGT	CCATTCAATC	CCTCCTTGAC	GAGGGGAAGC	AGTCCCTGAC	CAAGCTCGCA	120
GCGGCCTGGG	GCGGTAGCGG	TTCGGAAGCG	TACC			154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1          5          10          15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
          20          25          30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
          35          40          45
Glu Ala Tyr
          50

```

SECRET